Figure 1

DSP-12, 1656 Base Pairs

AAGCAGTGGTAACAACGCAGAGTACGCGGGCGAGGAGAATATCTTGCTGGGAGTGGACT
TTTCCAGTAAGGAAAGTAAAAGCTGCACCATTGGG**ATG**GTTCTCCGACTGTGGAGCGAC
ACGAAAATCCACCTTGATGGAGATGGTGGGTTCAGCGTGAGCACAGCAGGAAGGATGCA
CATATTTAAGCCTGTGTCTGTCCAGGCCATGTGGTCTGCCCTGCAGGTGCTTCACAAGG
CCTGCGAAGTGGCCCGGAGGCACAACTACTTCCCCGGGGGTGTAGCTCTCATCTGGGCT
ACCTACTATGAGAGCTGCATCAGCTCCGAGCAGAGCTGCATCAACGAGTGGAACGCCAT
GCAGGACCTGGAGTCTACGCGGCCCGACTCCCCCGCGCTATTTGTGGACAAGCCCACTG
AAGGGGAAAGGACCGAGCGCCTCATCAAAGCCAAGCTCCGAAGCATCATGATGAGCCAG
GATCTAGAAAATGTGACTTCCAAAGAGATTCGTAATGAATTAGAGAAACAGATGAATTG
TAACTTGAAGGAACTCAAGGAATTTATAGACAATGAGATGCTACTTATCTTGGGACAGA
TGGACAAGCCCTCCCTTATCTTCGATCATCTTTATCTCGGCTCTGAATGGAATGCATCC
AATCTGGAGGAACTGCAGGGCTCAGGGGTTGATTACATTTTAAATGTTACCAGAGAAAT
CGATAATTTTTTTCCTGGCTTATTTGCATATCATAACATCCGAGTCTACGATGAAGAGA
CCACAGACCTCCTCGCCCACTGGAATGAAGCGTATCATTTTATAAACAAAGCGAAGAGG
AACCATTCCAAGTGCCTGGTGCATTGCAAAATGGGCGTGAGTCGCTCGGCCTCCACAGT
CATAGCCTATGCAATGAAGGAATTCGGCTGGCCTCTGGAAAAAGCATATAACTATGTAA
AGCAGAAGCGCAGCATCACGCGCCCCAACGCGGGCTTTATGAGGCAGCTGTCTGAGTAT
GAAGGCATCTTGGATGCAAGCAAACAGCGGCACAACAAGCTGTGGCGTCAGCAGACAGA
CAGCAGCCTCCAGCAGCCTGTGGATGACCCTGCAGGACCTGGCGACTTCTTGCCAGAGA
CCCCAGATGGCACCCCGGAAAGCCAGCTGCCCTTCTTGGATGATGCCGCCCAGCCCGGC
TTAGGGCCCCCCCTCCCCTGCTGTTTCCGGCGACTCTCAGACCCCCTTCTGCCTTCCCC
TGAGGATGAAGCCGGCAGCTTGGTCCACCTGGAGGATCCGGAGAGGGAGGCTCTGTTGG
AGGAAGCTGCTCCACCTGCAGAGGTGCACAGGCCGGCCAGACAGCCCCAGCAAGGTTCC
GGACTCTGTGAGAAGGATGTGAAGAAGAAACTAGAGTTTGGGAGTCCCAAAGGTCGGAG
CGGCTCCTTGCTGCAGGTGGAGGAGACGGAAAGGGAGGAGGGCCTGGGAGCAGGGAGGT
GGGGGCAGCTTCCAACCCAGCTCGATCAAAACCTGCTCAACTCGGAGAACCTAAACAAC
AACAGCAAGAGGAGCTGTCCCAACGGCATGGAGGTAGGCAGAGCCCGGCCTGCAGGGTG
GCACACCCCATCCCTTCCATCCCACTCTAATTGGCCTACCTCAGCCTCTGTAGTAGGGA
CTACAGGCACCCGCCACCACACCCAGCTGATTTTTTTCTATTGTCTCCTCTGGGCCCCC
AGCTCCCATCTCCAGGGACCTGAGGGTTCTTTCACAGGG**TGA**TTCTGCTGGTGGGTACG
TAGTGCATACCTTATATAGCAAATTGAGAATCTGTTGGGAATAACACATATCTCTGCAC
ACCATCTTCACCCCATGTACCTTATTCATACCCTGGGCAGGGCTTCCAACTCAATTTCT
TTTTGTGTATGTAAAATTAAAACATATAATTTATCAGCCAAAAAAAAAAAAAAAAAAA
AA

Figure 2

DSP-12, 552 Amino Acids

MVLRLWSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFP
GGVALIWATYYESCISSEQSCINEWNAMQDLESTRPDSPALFVDKPTEGERTERLIKAK
LRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLY
LGSEWNASNLEELQGSGVDYILNVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAY
HFINKAKRNHSKCL**VHCKMGVSRS**ASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAG
FMRQLSEYEGILDASKQRHNKLWRQQTDSSLQQPVDDPAGPGDFLPETPDGTPESQLPF
LDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALLEEAAPPAEVHRP
ARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNL
LNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNWPTSASVVGTTGTRHHTQLIF
FYCLLWAPSSHLQGPEGSFTG

Figure 3

DSP-13, 1527 Base Pairs

CCTGGGAAGAAGTTATCTATCTCTCGAGTGACATTCAAGATATACCGTACCCCTCGGTTCTGTA
AGTCCTCTAAGTTGGAGGCATTCCATTCTGAGCCGGCCCC**ATG**ACCCTGAGCACGTTGGCCCGC
AAGAGGAAGGCGCCCCTCGCTTGCACCTGCAGCCTCGGTGGCCCCGACATGATTCCTTACTTCT
CCGCCAACGCGGTCATCTCGCAGAACGCCATCAACCAGCTCATCAGCGAGAGCTTTCTAACTGT
CAAAGGTGCTGCCCTTTTTCTACCACGGGGAAATGGCTCATCCACACCAAGAATCAGCCACAGA
CGGAACAAGCATGCAGGCGATCTCCAACAGCATCTCCAAGCAATGTTCATTTTACTCCGCCCAG
AAGACAACATCAGGCTGGCTGTAAGACTGGAAAGTACTTACCAGAATCGAACACGCTATATGGT
AGTGGTTTCAACTAATGGTAGACAAGACACTGAAGAAAGCATCGTCCTAGGAATGGATTTCTCC
TCTAATGACAGTAGCACTTGTACCATGGGCTTAGTTTTGCCTCTCTGGAGCGACACGCTAATTC
ATTTGGATGGTGATGGTGGGTTCAGTGTATCGACGGATAACAGAGTTCACATATTCAAACCTGT
ATCTGTGCAGGCAATGTGGTCTGCACTACAGAGCTTACACAAGGCTTGTGAAGTCGCCAGAGCG
CATAACTACTACCCAGGCAGCCTATTTCTCACTTGGGTGAGTTATTATGAGAGCCATATCAACT
CAGATCAATCCTCAGTCAATGAATGGAATGCAATGCAAGATGTACAGTCCCACCGGCCCGACTC
TCCAGCTCTCTTCACCGACATACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAA
TTAAGGGAGATCATGATGCAGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGT
TGGAAATGCAAATGGTGTGCAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGT
GATCCTTGGTCAAATGGATAGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGG
AATGCCTCCAACTTAGAGGACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAG
AGATAGATAACTTCTTCCCAGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGC
AACGGATCTCCTGGCGTACTGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGA
TCTAAATGCCTTGTGCACTGCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATG
CAATGAAGGAATATGGCTGGAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGT
AACCAAGCCCAACCCAAGCTTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGC
TTCCTAGGCTTGATTCATGGAGGGAGGGACAAGCCCTGGGGAGAGAAAAGCACAGAATTTGAGT
CAGTAGATCTGGTTTCCATTCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACAT
TTCTCATCCTTACCTGACCCCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATT
GTGAATAAAAATGTGTTTGAATGTTTATAAAAAAAAAAAAAAAAAA

Figure 4

DSP-13, 509 Amino Acids

MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGS
STPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNRTRYMVVVSTNGRQDTEES
IVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLH
KACEVARAHNYYPGSLFLTWVSYYESHINSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERER
TERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFE
HVFLGSEWNASNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKF
ISKAKKHGSKCL**VHCKMGVSRS**ASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEE
YQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

Figure 5

A **DSP13 Alternate Splice Variant, 723 Base Pairs**

CTGCCCGGCTTCTAACAGGCCACTGACCGGTACTCACTGGGGACCCACGCTCTAAGTTGTTGAT
CTCTAGAACCGATTTTGGAAAAGGATTTGCCTTATTGAAGAAGACAGGATCATTCTTCTTTCTT
TCCCATTTAAGAATAATCGTTATTAAGAATATCGTTTAAGAATAATCGTTATTTCTCTCTTCTC
AGACCTACTGAACGTGAACGAACAGAAAGGCTAATTAAAACCAAATTAAGGGAGATC**ATG**ATGC
AGAAGGATTTGGAGAATATTACATCCAAAGAGATAAGAACAGAGTTGGAAATGCAAATGGTGTG
CAACTTGCGGGAATTCAAGGAATTTATAGACAATGAAATGATAGTGATCCTTGGTCAAATGGAT
AGCCCTACACAGATATTTGAGCATGTGTTCCTGGGCTCAGAATGGAATGCCTCCAACTTAGAGG
ACTTACAGAACCGAGGGGTACGGTATATCTTGAATGTCACTCGAGAGATAGATAACTTCTTCCC
AGGAGTCTTTGAGTATCATAACATTCGGGTATATGATGAAGAGGCAACGGATCTCCTGGCGTAC
TGGAATGACACTTACAAATTCATCTCTAAAGCAAAGAAACATGGATCTAAATGCCTTGTGCACT
GCAAAATGGGGGTGAGTCGCTCAGCCTCCACCGTGATTGCCTATGCAATGAAGGAATATGGCTG
GAATCTGGACCGAGCCTATGACTATGTGAAAGAAAGACGAACGGTAACCAAGCCCAACCCAAGC
TTCATGAGACAACTGGAAGAGTATCAGGGGATCTTGCTGGCAAGCTTCCTAGGCTTGATTCATG
GAGGGAGGGACAAGCCCTGGGGAGAGAAAAGCACAGAATTTGAGTCAGTAGATCTGGTTTCCAT
TCCTGGTTCACCCTCTTGCTGCAACCCTGAGAAGTTACTTCACATTTCTCATCCTTACCTGACC
CCATCTATAAAA**TGA**AAATCAAGAGATCCATCTCACAGGGTTATTGTGAATAAAAATGTGTTTG
AATGTTTATAAAAAAAAAAAAAAAAAA

B **DSP13 Alternate Splice Variant, 241 Amino Acids**

MMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASN
LEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCL
VHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFLGL
IHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

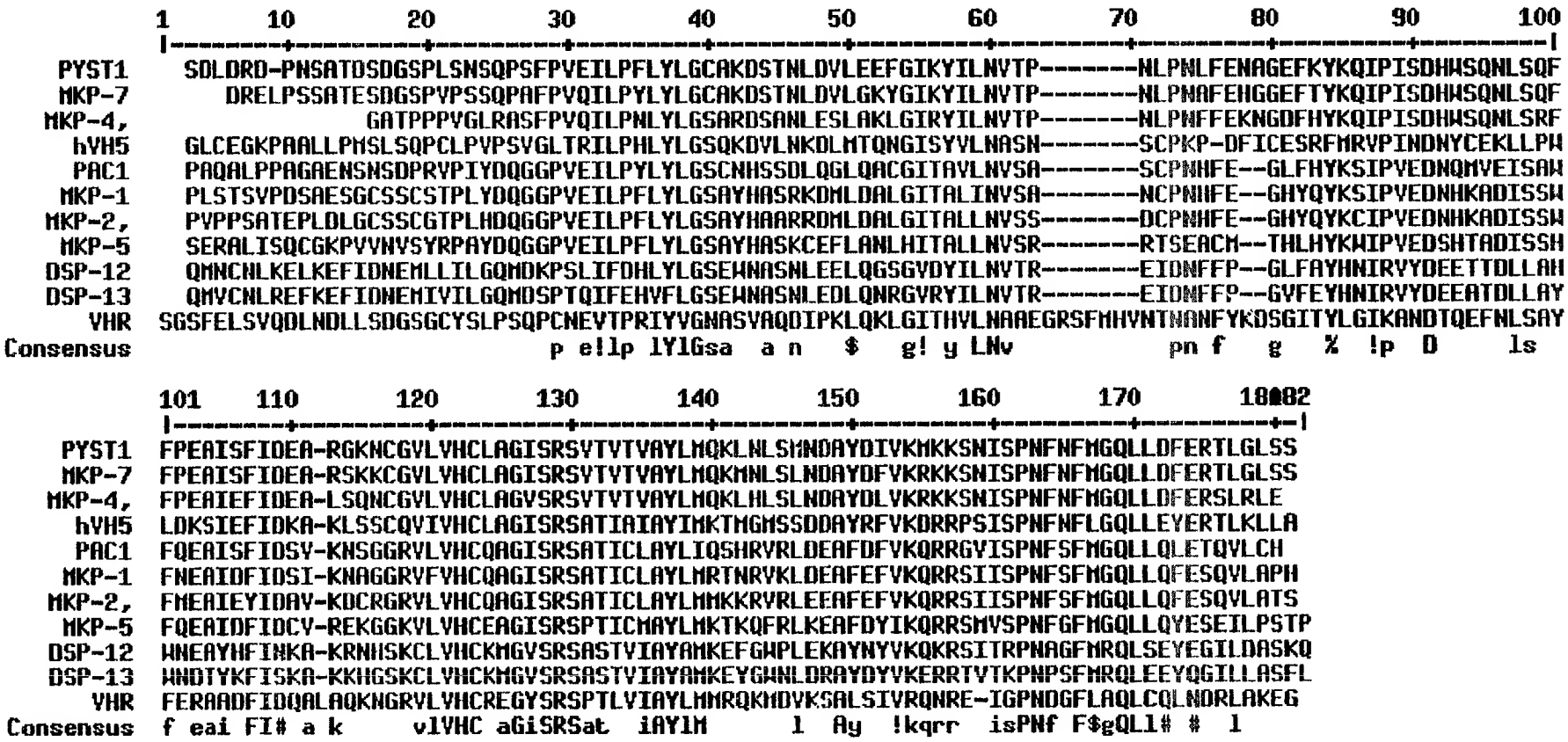
1 10 20 30 40 50 60 70 80 90 100
PYST1 SDLDRD-PNSATDSDGSPLSNSQPSFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTP-------NLPNLFENAGEFKYKQIPISDHWSQNLSQF
MKP-7 DRELPSSATESDGSPVPSSQPAFPVQILPYLYLGCAKDSTNLDVLGKYGIKYILNVTP-------NLPNAFEHGGEFTYKQIPISDHWSQNLSQF
MKP-4, GATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTP-------NLPNFFEKNGDFHYKQIPISDHWSQNLSRF
hVH5 GLCEGKPAALLPHSLSQPCLPVPSVGLTRILPHLYLGSQKDVLNKDLMTQNGISYVLNASN-------SCPKP-DFICESRFMRVPINDNYCEKLLPK
PAC1 PAQALPPAGAENSNSDPRVPIYDQGGPVEILPYLYLGSCNHSSDLQGLQACGITAVLNVSA-------SCPNHFE--GLFHYKSIPVEDNQMVEISAK
MKP-1 PLSTSVPDSAESGCSSCSTPLYDQGGPVEILPFLYLGSAYHASRKDMLDALGITALINVSA-------NCPNHFE--GHYQYKSIPVEDNHKADISSW
MKP-2, PVPPSATEPLDLGCSSCGTPLHDQGGPVEILPFLYLGSAYHAARRDMLDALGITALLNVSS-------DCPNHFE--GHYQYKCIPVEDNHKADISSW
MKP-5 SERALISQCGKPVVNVSYRPAYDQGGPVEILPFLYLGSAYHASKCEFLANLHITALLNVSR-------RTSEACM--THLHYKWIPVEDSHTADISSH
DSP-12 QMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNASNLEELQGSGVDYILNVTR-------EIDNFFP--GLFAYHNIRVYDEETTDLLAK
DSP-13 QMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNASNLEDLQNRGVRYILNVTR-------EIDNFFP--GVFEYHNIRVYDEEATDLLAY
VHR SGSFELSVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAY
Consensus p e!lp lYlGsa a n $ g! y LNv pn f g % !p D ls
101 110 120 130 140 150 160 170 180 182
PYST1 FPEAISFIDEA-RGKNCGVLVHCLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTLGLSS
MKP-7 FPEAISFIDEA-RSKKCGVLVHCLAGISRSVTVTVAYLMQKMNLSLNDAYDFVKRKKSNISPNFNFMGQLLDFERTLGLSS
MKP-4, FPEAIEFIDEA-LSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLVKRKKSNISPNFNFMGQLLDFERSLRLE
hVH5 LDKSIEFIDKA-KLSSCQVIVHCLAGISRSATIAIAYIMKTMGMSSDDAYRFVKDRRPSISPNFNFLGQLLEYERTLKLLA
PAC1 FQEAISFIDSV-KNSGGRVLVHCQAGISRSATICLAYLIQSHRVRLDEAFDFVKQRRGVISPNFSFMGQLLQLETQVLCH
MKP-1 FNEAIDFIDSI-KNAGGRVFVHCQAGISRSATICLAYLMRTNRVKLDEAFEFVKQRRSIISPNFSFMGQLLQFESQVLAPH
MKP-2, FMEAIEYIDAV-KDCRGRVLVHCQAGISRSATICLAYLMKKRVRLEEAFEFVKQRRSIISPNFSFMGQLLQFESQVLATS
MKP-5 FQEAIDFIDCV-REKGGKVLVHCEAGISRSPTICMAYLMKTKQFRLKEAFDYIKQRRSMVSPNFGFMGQLLQYESEILPSTP
DSP-12 WNEAYHFINKA-KRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNAGFMRQLSEYEGILDASKQ
DSP-13 WNDTYKFISKA-KKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNPSFMRQLEEYQGILLASFL
VHR FERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNRE-IGPNDGFLAQLCQLNDRLAKEG
Consensus f eai FI# a k vlVHC aGiSRSat iAYlM l Ay !kqrr isPNf F$gQLl# # l

Figure 6

Alignment of DSP-12 and DSP-13

```
        1        10        20        30        40        50        60        70        80        90       100       110
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-13  MTLSTLARKRKAPLACTCSLGGPDMIPYFSANAVISQNAINQLISESFLTVKGAALFLPRGNGSSTPRISHRRNKHAGDLQQHLQAMFILLRPEDNIRLAVRLESTYQNR

        111      120       130       140       150       160       170       180       190       200       210       220
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-12                                          MVLRLHSDTKIHLDGDGGFSVSTAGRMHIFKPVSVQAMWSALQVLHKACEVARRHNYFPGGVALIWATYYESCI
DSP-13  TRYMVVVSTNGRQDTLESIVLGMDFSSNDSSTCTMGLVLPLWSDTLIHLDGDGGFSVSTDNRVHIFKPVSVQAMWSALQSLHKACEVARAHNYYPGSLFLTWVSYYESHI

        221      230       240       250       260       270       280       290       300       310       320       330
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-12  SSEQSCINEWNAMQDIESTRPDSPALFVDKPTEGERTERLIKAKLRSIMMSQDLENVTSKEIRNELEKQMNCNLKELKEFIDNEMLLILGQMDKPSLIFDHLYLGSEWNA
DSP-13  NSDQSSVNEWNAMQDVQSHRPDSPALFTDIPTERERTERLIKTKLREIMMQKDLENITSKEIRTELEMQMVCNLREFKEFIDNEMIVILGQMDSPTQIFEHVFLGSEWNA

        331      340       350       360       370       380       390       400       410       420       430       440
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-12  SNLEELQGSGVDYIIHVTREIDNFFPGLFAYHNIRVYDEETTDLLAHWNEAYHFINKAKRNHSKCLVHCKMGVSRSASTVIAYAMKEFGWPLEKAYNYVKQKRSITRPNA
DSP-13  SNLEDLQNRGVRYILNVTREIDNFFPGVFEYHNIRVYDEEATDLLAYWNDTYKFISKAKKHGSKCLVHCKMGVSRSASTVIAYAMKEYGWNLDRAYDYVKERRTVTKPNP

        441      450       460       470       480       490       500       510       520       530       540       550
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-12  GFMRQLSEYEGILDASKQR--HNKLWRQQTDSSLQ-QPVDDPAGPGDFLPETPDGTPESQLPFLDDAAQPGLGPPLPCCFRRLSDPLLPSPEDEAGSLVHLEDPEREALL
DSP-13  SFMRQLEEYQGILLASFLGLIHGGRDKPWGEKSTEFESVDLVSIPGSPSCCNPEKLLHISHPYLTPSIK

        551      560       570       580       590       600       610       620       630       640       650       660
        |--------+---------+---------+---------+---------+---------+---------+---------+---------+---------+----------|
DSP-12  EEAAPPAEVHRPARQPQQGSGLCEKDVKKKLEFGSPKGRSGSLLQVEETEREEGLGAGRWGQLPTQLDQNLLNSENLNNNSKRSCPNGMEVGRARPAGWHTPSLPSHSNW

        661      670       680       690       701
        |--------+---------+---------+----------+|
DSP-12  PTSASVVGTTGTRHHTQLIFFYCLLWAPSSHLQGPEGSFTG
```

Figure 7